## REMARKS

Claims 12-22 are now pending, with claim 12 being the sole independent claim.

Claims 1-11 have been canceled without prejudice to or disclaimer of the subject matter recited therein.

Claims 12-22 have been added. Support for the reference to "histone deacetylase activity" in claim 12 is found at least in the paragraph at page 1, lines 10-27, of the specification. Support for the sequence identity and the Clustal default parameters recited in claim 12 is found at least in the paragraph at page 4, lines 24-35 of the specification. Support for the use of the term "recombinant" in claims 16, 18, and 20-22, is found at least in the paragraph at page 8, lines 33-36 of the specification. Support for claims 19-21 is found at least in Examples 4-5, pages 16-20, of the specification. Support in the specification for claim 22 is found at least in the paragraph at page 2, lines 20-25. No new matter has been added.

The specification has been amended at two locations to remove reference to the following URL: www.ncbi.nlm.nih.gov/BLAST/.

## RESPONSE TO RESTRICTION REQUIREMENT

In response to the Restriction Requirement in the Office Action mailed November 5, 2002, Applicants hereby elect, without traverse, Group I, claims 1-5, 7, 10, and 11 drawn to an isolated nucleic acid fragment encoding a histone deacetylase 1 protein, transformed host cell comprising said nucleic acid and method of expressing said nucleic acid. In addition, Applicants hereby elect invention B, to SEQ ID NO:3 or a sequence encoding SEQ ID NO:4; wherein SEQ ID NO:4 is an amino acid sequence encoded by nucleotides 130-1548 of SEQ ID NO:3. Applicants submit that now pending Claims 12-22 are directed to Group IB.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,

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## VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown within brackets, and inserted material is shown underlined.

## IN THE SPECIFICATION:

**Paragraph beginning at page 4, line 36, and continuing through page 5, line 20:**

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

**Paragraph at page 15, lines 5-21:**

cDNA clones encoding chromatin associated proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nature Genetics 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.